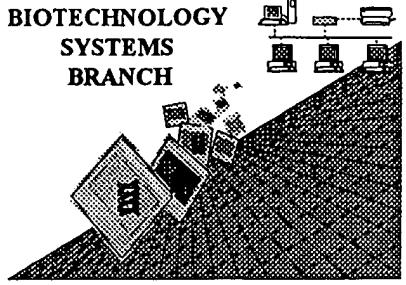


RAW SEQUENCE LISTING

ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/423,545
Art Unit / Team No.: 1646
Date Processed by STIC: 2/28/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

RECEIVED
MAR - 9 2000
TC 1600 MAIL ROOM

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/423,545</u>
1 <input checked="" type="checkbox"/> ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE Wrapped Nucleic	<p>The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>	
2 <input type="checkbox"/> Wrapped Aminos	<p>The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>	
3 <input type="checkbox"/> Incorrect Line Length	<p>The rules require that a line not exceed 72 characters in length. This includes spaces.</p>	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	<p>The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.</p>	
5 <input type="checkbox"/> Non-ASCII	<p>This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.</p>	
6 <input type="checkbox"/> Variable Length	<p>Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.</p>	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	<p>A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.</p>	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	<p>Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped</p> <p>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).</p>	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	<p>Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000</p>	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	<p>Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</p>	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	<p>Sequence(s) _____ are missing this mandatory field or its response.</p>	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	<p>Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)</p>	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	<p>Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.</p>	

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HAR-9 2000
TC 1600 MAIL ROOM

NA

1646

PAGE : 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545

DATE: 02/28/2000
TIME: 16:34:20

Input Set: I423545.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

1 <110> Kenji SHIBATA
2 Motoo YAMASAKI
3 Tetsuo YOSHIDA
4 Tamio MIZUKAMI
5 Akeo SHINKAI
6 Hideharu ANAZAWA
7 <120> Peptides having a cyclic structure and restoring the
8 activities of P53 protein to mutant P53 protein
9 <130> 1061
10 <140> US/09/423,545
11 <141> 1999-11-12
12 <150> JP97/126113
13 <151> 1997-05-15
14 <160> 32

Doc
Correct

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

E--> 15 <210> 8
16 <211> 32
17 <212> DNA
18 <213> Artificial Sequence
19 <220>
20 <223> Other nucleic acid Synthetic DNA
21 <400> 8
E--> 22 CTAGACAGCC AGACTGCCTT CGGGTCACT GC
23 32

under new Sequence (see item 1 on Error Summary sheet)
Rules, all bases
need to be in lower-case - format error
↓ letters
32

24 <210> 9
E--> 25 <211> 32
26 <212> DNA
27 <213> Artificial Sequence
28 <220>
29 <223> Other nucleic acid Synthetic DNA
30 100 9

E--> 31 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
32 32

E--> 33 <210> 10
34 <211> 26
35 <212> DNA
36 <213> Artificial Sequence
37 <220>

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545DATE: 02/28/2000
TIME: 16:34:20

Input Set: I423545.RAW

38 <223> Other nucleic acid Synthetic DNA
39 <400> 10
E--> 40 TCGAGAGACA TGCCTAGACA TGCCTG
41 26

42 <210> 11
E--> 43 <211> 26
44 <212> DNA
45 <213> Artificial Sequence
46 <220>
47 <223> Other nucleic acid Synthetic DNA
48 <400> 11
E--> 49 TCGACAGGCA TGTCTAGGCA TGTCTC
50 26

51 <210> 12
E--> 52 <211> 22
53 <212> DNA
54 <213> Artificial Sequence
55 <220>
56 <223> Other nucleic acid Synthetic DNA
57 <400> 12
E--> 58 TCGAGCCCGG GGGTACCGCA TG
59 22

60 <210> 13
E--> 61 <211> 14
62 <212> DNA
63 <213> Artificial Sequence
64 <220>
65 <223> Other nucleic acid Synthetic DNA
66 <400> 13
E--> 67 CGGTACCCCC GGGC
68 14

69 <210> 14
E--> 70 <211> 32
71 <212> DNA
72 <213> Artificial Sequence
73 <220>
74 <223> Other nucleic acid Synthetic DNA
75 <400> 14
E--> 76 TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
77 32

78 <210> 15
E--> 79 <211> 32
80 <212> DNA
81 <213> Artificial Sequence
82 <220>

format error

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545DATE: 02/28/2000
TIME: 16:34:20

Input Set: I423545.RAW

83 <223> Other nucleic acid Synthetic DNA
 84 <400> 15
 E--> 85 GTACCGCTCGA CAGGCAAGTC CAGGCAAGTC CC
 86 32

E--> 87 <210> 24
 88 <211> (16) 15 shown
 89 <212> PRT
 90 <213> Artificial Sequence
 91 <220>
 92 <221> BINDING
 93 <222> (7) .. (13)
 94 <223> BINDING type is -CONH2-.
 95 <220>
 96 <221> SITE
 97 <222> (15)
 98 <223> Xaa represents L-Leucine amide.
 99 <220>
 100 <223> Synthetic peptide
 101 <400> 24

W--> 102 Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser Arg His Lys Lys Xaa
 103 1 5 10 15

more amino acid
 numbers directly
 under pertinent amino
 acid. DO NOT use TAB
 codes between numbers; use
 space characters.

PTI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I423545.RAW

Line ? Error/Warning

Original Text

16 E Input 32, Calc# Bases 0 differ
 22 E Wrong Amino Acid Designator
 25 E Input 32, Calc# Bases 0 differ
 31 E Wrong Amino Acid Designator
 34 E Input 26, Calc# Bases 0 differ
 40 E Wrong Amino Acid Designator
 40 E Wrong Amino Acid Designator
 40 E Wrong Amino Acid Designator
 43 E Input 26, Calc# Bases 0 differ
 49 E Wrong Amino Acid Designator
 49 E Wrong Amino Acid Designator
 49 E Wrong Amino Acid Designator
 52 E Input 22, Calc# Bases 0 differ
 58 E Wrong Amino Acid Designator
 58 E Wrong Amino Acid Designator
 61 E Input 14, Calc# Bases 0 differ
 67 E Wrong Amino Acid Designator
 67 E Wrong Amino Acid Designator
 70 E Input 32, Calc# Bases 0 differ
 76 E Wrong Amino Acid Designator
 79 E Input 32, Calc# Bases 0 differ
 85 E Wrong Amino Acid Designator
 88 E Input 16, Calc Seq.Length 15 differ
 102 W "N" or "Xaa" used: Feature required

<211> 32
 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
 <211> 32
 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
 <211> 26
 TCGAGAGACA TGCCTAGACA TGCCTG
 TCGAGAGACA TGCCTAGACA TGCCTG
 TCGAGAGACA TGCCTAGACA TGCCTG
 <211> 26
 TCGACAGGCA TGTCTAGGCA TGTCTC
 TCGACAGGCA TGTCTAGGCA TGTCTC
 TCGACAGGCA TGTCTAGGCA TGTCTC
 <211> 22
 TCGAGCCCGG GGGTACCGCA TG
 TCGAGCCCGG GGGTACCGCA TG
 TCGAGCCCGG GGGTACCGCA TG
 <211> 14
 CGGTACCCCC GGGC
 CGGTACCCCC GGGC
 <211> 32
 TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
 TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
 TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
 TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
 <211> 32
 GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
 GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
 GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
 GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
 <211> 16
 Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser A